

FIGURE 1

CDC27A1 Gene Structure

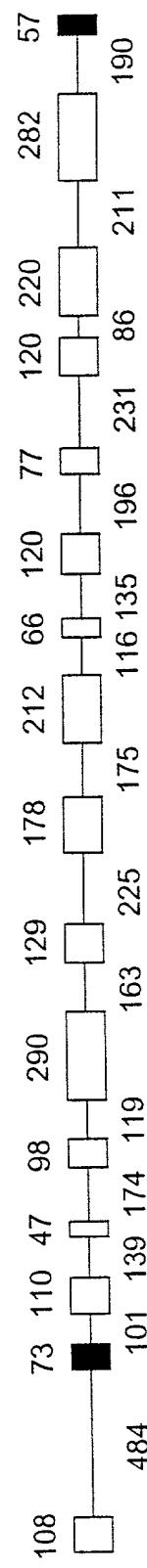


FIGURE 2

Fig. 3

1 ATGTCAGAAAATCGGAACCGCGTCAACTCGAGAATTCTACA
1 TCTAAAGTGTCTAAACGTTACAGTCTTTGAGCCTGGCGCAGTTGAGCTCTTAAGATGT
1 M S E N S E P R Q L E N S T -
1 GCCGGAAGAGAGCTCATTCCTCTTAGTCCCACCAATTCAAGACGGCAACGACGACCTAAC
1 CGGCCTTCTCTCGAGTAAGGAGAATCAGGGTGGTTAAGTCTGCCGTGCTGCTGGAATTG
1 A G R E L I P L S P T N S D G N D D L N -
1 TATCATCTGCATGCTTTGAGTTATCTCGTCTCTACTTTCTCTGGTCATCCAGAAATCT
121 ATAGTAGACGTACGAAAATCAATAGACCAAGGGATGAAAGAAGACCAAGTAGGTCTTACA
121 Y H L H A F E L S R L L L S S G H P E S -
121 GTTATAGATCTTCTCAAAGTGTACATACTTCCAAGGTTCTCTAATCTCGTCAAATAT
181 CAATATCTAGAAAGAAGTTTACATGTATGAAGGTTCCAAGAGGATTAGAGCAGTTATA
181 V I D L S S K C T Y F Q G S P N L V K Y -
181 CTTTGCTCGATCCCTAATTCTCTATTCCCTTGCCGAAGATGGCTTCACTGTGACTCTC
241 GAAACGAGCTAGGGATTAAGAGGATAAAGGGAACGGCTTCTACCGAAGTGACACTGAGAG
241 L C S I P N S P I S L A E D G F T V T L -
241 TCGCCTGAGTCTCCCTCCGCTCCGGCTAGTTCCGCTGTAGTTGGATTTCGAGGAAAT
301 AGCGGACTCAGAGGGAGGCCAGGCCATCAAAGCGACATCAAACCTAAACGTCCTTTTA
301 S P E S P S A P A S F A C S L D L Q E N -
301 GTTGTGTTAGAACAGTTATGGATCCGAGATCTCTCACGCTAAAGCATTGAGAGAGAAT
361 CAACACAATCTTGTCAAATACCTAGGCTCTAGAGAGTGCGATTCTGTAAGCTCTCTTTA
361 V V L E Q F M D P R S L T L K H S R E N -
421 GCGGAACAAGAGGGAGCTAGAGCTCATGCCATTGCCAAAAGAAGTCGAAATGATGAAAC
421 CGCCCTTGGTCTCCTCGATCTCGACTACGGTAACGGTTTCTCAGCTTTACTACCTTG
421 A E Q E E L E L M P L P K R S R N D G N -

43
 GATGTGATTACTCTGTAATAGTAGCGACCTAACCACTCGAACTGGTGGCTGGGA
 481
 CAAACCTTAATGAGACATTCATCGCTGGATTCTGAGCTTGACAAACGGACACCT
 43
 D V N Y S V I D S R P N D I R T V A C G -
 541
 ACTATGCTTGGACTAATTACCTTGAATCCCACGTTGGTTGATTTAAGTGC
 541
 TGATAACGAAACCTGATAAAATCGAGAACTAGGCTTGAACCCAAAAGCTAAATTACGT
 T M I G T I L A I E S Q A S V F N I S A -
 601
 TCTAACCGAGGAATAGACGGTTTGTCAAGATCATCGCCTGGTCCGAGACATCCAAAT
 601
 AGATTTGGCTCCCTATCTCCGAAAACIAGTTCTAGTACTCGGACCCGGCTCTGAGCTTA
 S N R G I E A F V Q D H Q P G P Q T S N -
 661
 GCCTCACTGGATGTCAATCTCACACTCCGTTAGAGGAAACCGAGAACCCATTGGCCTCT
 661
 CGAAAGTCACCTACAGTTAGGATGTGTAGCCATCTCTTCTTCTTGTAAACGGTAA
 A S V D V N P T H R I E E S K N D L P S -
 721
 CCTCAGGAGGATGGATATTACGAGCGACCTGAAATTGGAGATTCTCAAATGGTCAAC
 721
 GGAGTCCTCCTACCTATAATGCTCGCTGGACTTTAACCTCTAAAGGTTAACGACTGTG
 P Q E D G Y Y E R P E I G D F Q I A D N -
 781
 CAAATATTAATCGAACAGGTGATGNTAAAATAAGAACGGATCTCTCCCTAACGGCAG
 781
 GTTATAATTAGCTTCTCCACTACTATTTTATCTTCTAGAACGGGATTCCTCTC
 Q I L I E E G D D K N K K D L F P K G E -
 841
 ATACAAACTGATTCTGCGACTCCGATCCCGTTGCCTCATGATGCCAACAGAAATGAG
 841
 TATGTTGACTAACGACACGTCAGGCTAGGGCAACGGAGTAACACGGTTGTCTTACTC
 I Q T D S V Q S D P V A S L M P T E N E -
 901
 TTAGAACCACTGCAAGATTGGGATGACACTGAAGATCTACTCTAGATGATCACACTGTA
 901
 AATCTGGTCACGTCACACACTACTGTGACTTCTAGATGAACATCTACTAGTGTGACAT
 L E P V Q I V D D T E D L L V D D H T V -
 961
 GACATCGTTAGCACCCCTGACAGAGAGCTGCCGTTGAGCTTCTGCTACAGAACGAAAT
 961
 CTGTAGCAATCGTGGGACTGTCTCTCAACGGCAACTCGGAAGACGATGTCTCGATTA
 D I V S T P D R E L P L K P S A T E A N -
 1021
 CAACATAAAATCTTGGTACAAAAAAACTCTGGATCAATGCAATTGCCGGAAACAGCAAA
 1021
 GTTCTATTAGAAACCATGTTTTGAGACCTAGTTACGGCCCTTGTCTGTT

Q D K S E V Q K T I D Q C K L P G N S K -
 ACGTACAGCTGTTCCCTGAGATAAAACACACCAGAAAAAGTAAAGTTATCCAGAAGAGG
 1081 -----+----- 1140
 TCCATGTGCGACAAGGGGACTCTATTTTGTTGGTCCTTTTCAATTCAATAGGCTCTCC
 T Y S C S P E I K H T R K S K V I Q K R -
 AACCAGAATTAAACACCGTTCTTAACAGTCAGAGCATAGGCAAAGCCTAACACT
 1141 -----+----- 1200
 TTCTGCTTAAATTGTGCCAAGCAGAATTCTAGTCTCTAGTCGGTTCTATTGTG
 314 K Q N F N T V R L K D Q K | D Q A K H N T -
 ATTCCAGATTTGATTCTTACACTATTGTAGAGGAAGAAGGTTCAAGTGGCTACGGATT
 1201 -----+----- 1260
 TAAGGTCTAAAACAAAGAATGTGATAACATCTCTTCTCCAGTCCACCGATGCCCTAA
 I P D F D S Y T I V E E E G S G | G Y G I -
 GTTTATAAGGAAACGAGGAAACTGATGGAACAGACTTGCATTAAATGCCCTCATGTT
 1261 -----+----- 1320
 CAAATATTCCGTTGCTCTTGTACTACCTTGTCTAACGTTAACGGAGTACAA
 516 V Y K A T R K T D G T E F A I K | C P H V -
 GGCGCTCAGAAGTATTATGTGAATAATGAAATCAGAATGCTGGAGCGTTGGGGGAAA
 1321 -----+----- 1380
 CGCGGAGTCTICATAATACACTTATTACTTTAGTCTTACGACCTCGAAAACCCCCCTTT
 617 G A Q K Y Y V N N E I R M L E R F G | G K -
 AACTGTATAATAAGCATGAAGGCTGTCTCAAGAATGGAGATTCTGATTGCATCATCTT
 1381 -----+----- 1440
 TTGACATATTATTCGTAACCTCCGACAGAGTTCTACCTCTAACACTAACGTTAGGAA
 N C I I K H E G C L K N G D S D C I I L -
 GAGCACCTTGAACATGACAGACCTGATTCAATTGAAGAGAGAAATAGATGTGTATCAGCTG
 1441 -----+----- 1500
 CTCGTGGAACCTGTACTGTCTGGACTAACGTTCTCTCTTATCTACACATAGTCAC
 E H L E H D R P D S L K R E I D V Y Q L -
 718 CAGTGGTACGGCTACTGCATGTTCAAAGCTCTATCGAGTCAGCATAAGCAGGGTGTGTT
 1501 -----+----- 1560
 GTCACCATGCCGATGACGTACAAGTTGAGATAGCTCAGACCTATTGTCGGCCACAA
 718 Q W Y G Y C M F K A L S S L H K Q | G V V -
 CATAGGGATGTTAACGCCAGGAAACTTCCTCTCTAGGAAGACCAACAAAGGCTATCTC
 1561 -----+----- 1620
 GTATCCCTACAAATTGGTCTTGAAGGAGAAGAGATCTTCTGGTTGTTCCGATAGAG
 H R D V K P G N F L F S R K T N K G Y L -
 819 ATTGATTTAACCTGCCATGATTGGACAGAAGTACAGAACGGCAGATAAATCAAAA
 910

1621 TAAC TAA AATTGGAACCGTACCTAACGTGGCTTCATGCTCTCGTCTATTAGTTT
 I D E N L A M | D L H Q K Y R R A D | K S K -
 1681 CGACCTTCAGGTCTTCCTACGGCCAGCAAGAAACCTCATTCATGGTTAAATCAGTCAT
 CTCGAAGTCCAGAAGGAATGGCGGTCTTGTACTATGTAACCATTAGTGAGGAA
 A A S G L P T A S K K H E T L V K S L D -
 GCGGTAAACCCAGGGACCAACAAACCTTCAGAAAACCTTAGGCCCTAATAGTATCAAG
 1741 CGCCATTGGCTCCCTGGTTGGAAAGAGCTTTGAAATCCCCATTATCATAGTTC
 A V N R G T N K P S Q K T L A P N S I K -
 AAAGCAGCGGGAAAGACAGAGCTCGGAATGACATGACAGATGGGAGAGACTCAATAGC
 1801 TTTCGTGCGCCCTTCTGTTCTCGAGCCCTACTGTACTGGCTTACCTCTCTGAGTTATCG
 K A A G K T R A R N D M T R W E R L N S -
 CAAGGGGCAGAAGGGCTGGCTTAACTTCAGCTAAAGATGTGACCAAGCAAGGAAACAAC
 1861 GTTCCCCCTCTTCCCAGACCGAATTGAGTCGTTTCTACACTGGCTGTCTTGTG
 Q G A E G S G L T S A K D V T S T R N N -
 CCTTCAGGTGAAAAGAGAACAGACAGCCCTTGGCATGTCATGGAGAAAAGCCCTTTAGAT
 1921 GGAAGTCCACTTTCTCTCTCGAAACGGTACACTACCTTCTTGGCAAATCTA
 P S G E K R R E P L P C H G R K A D L D -
 TTCTGCAAGAGACAAATGTCGTTCCAATTCCAAACCATGAAGTATCATCCAAAGCTCCT
 1981 AAAGACGTTCTGTCAGACAAGGTTAGGTTGGTACTTCATAGTAGGTTGGAGGA
 F L Q E T M S V P I P N H E V S S K A P -
 ACGTCTATGAGAAAACGGGTAGCTGCTTCCAGGGAAAGCTGAGAACGAACTTCTTAT
 2041 TGCAAGATACTCTTGGCCATGACAGAACGGTCCCTTCGACTCTTCTTGAAGAAATA
 T S M R K R V A A L P G K A E K E L L Y -
 CTGACCCCAATGCCACTGTGCTCTAACGGTCGGCCTGAACCGAGGGACGTAATTGAGAAG
 2101 GACTGGGGTTACGGTGACACGAGATTGCCAGCCGGACTTCGTCCTTGAAGAAATA
 L T P M P L C S N G R P E A G | D V I E K -
 AAAGACGGTCCTTGCCTAGGAACCAAAAGGCTTCCGAGCTCCAGAGGTTGGCTTCAGATCT
 2161 TTTCTGCCAGGAACCAAGTCCTTGGTTCCGAAAGGCTCGAGETCTCTAACGAAGTCTAGA
 K D G P C S G T K G F R A P E | V C F R S -

TTGCACTAAGGACCTAAGATAACGTGTGGCTGGGGAGTTAC~~T~~^TGTATAACCTGATA
 2221 AACGTGGTCCCTGGATTCTATCTGCACACCAAGACGCCCTCAATGAAACATAATGGAGTAT
 I H Q G P K I D V W S A G V T L L Y L I -
 12 13
 ATGGGAAGGACACCTTTCACTGGTGACCCCTGAACAGAACATAAAAGGACATTGGCACAACTA
 2281 TACCCCTTCCTGGAAAGTGACCACTGGACTTGTCTTGTATTTCCTGGTACGTGTTGAT
 12 13
 M G R T P F T G D P E Q N I K D S A Q L -
 CGAGGCAGTGAAGAATTATGGGAAGTAGCCAAGCTGCACAACCGTGAATCCCTTTCCCT
 2341 GCTCCGTCACITCTTAATACCCCTCATCGGTTGACGTGTTGGCACTTAGGAGAAAGGGA
 R G S E E L W E V A K L H N R E S S S F P -
 13 14
 AACGAATTATACGGACTAAGGTACTTGAAGGGATGGAGTTGAGAAAATGGTGCAGAACTC
 2401 TTCCCTTAATATGCTAGTICCATGAACCTCCCCTACCTCAACTCTTTTACCAAGCTTCAAG
 13 14
 K E L Y E S R Y L K G M S I R K W C E L -
 AACACAAAACGGAGAGAGTTCTAGACGTAATTCCACTATCGCTTCTTGAACCTCGTTGAT
 2461 TTGTGTTTGGGTCTCTCAAAGATCTGCATTAAGGTGATAGCGAAGAACTGGAGCAACTA
 N T K R R E F L D V I P L S L L D L V D -
 AAATGTTGACCGTTAACCGAGGGGACGAATCAGGGCAGAGGATGCTCTCAAGCACCAC
 2521 TTTACAAACTGGCAATTGGGCTCCGCTGCTTAGTCGGCTCTCTACGAGAGTTCGTGTGCTG
 K C L T V N P R R R I S A E D A L K H D -
 TTCTTCCATCCACTACATGAAACCCCTAGAAACCAAAATGCTCTTAAACAGCAGCCTACA
 2581 AAGAAGGTAGGTCTGTACTTTGGAAATCTTGGTTACGAGGAATTGTCGTGGATGT
 F F H P V H E T L R N Q M L L K Q Q P T -
 GTGGTTGCTGACGGAGTAAGCCAAACTCTAAACTATTTACAATTGTAAGTAAAGTAAAG
 2641 CACCAACGACTGCCTCATTCGGTTGAGAATTGATAAAATGTTAACATTTCATTATTC
 V V A D A V S Q T L N Y L Q L *

Fig. 4

1 CCGCTGTAATGGTGTGTCGGAGGCCTTGTTGTTAGCTAACAGGCACTAA 60
61 ATGATGGAGAATCTACTGGGAATTGTGTCCAGAAAAACCTT 120
61 CCAGTAGTAGTAGTAGCTACTACCTCTTAGATGACCCCTTAACACAGGTCTTTTGGAA
61 | M M E N L L A N C V Q K N I
61 AACCATTTATGTCACCAATGCTATCTTCCCTTGGAACTTCTTCGCCGAATTCCA 180
121 TTGGTAAAATAACAAGTGGTTACGATAGAAGGAAACGCTTGAAGAAGAGCAGGGTTAAAGCT
121 N H F M E T N A I F L C E L D L A Q F P
121 TCTGAGGTCAACCTGCAATTGTTAGCCAGGTGTTACTTGAGTAACAGTCAGCTTATAGT 240
181 AGACTCCACTTGGACGTTAACAAATCGGTCCACAAATGAACACTCAATTGTCAGTCGAATATCA
181 S E V N L Q L I A R C Y L S N S Q A Y S
181 43 GCATATTATATCCTTAAAGGTTCAAAACGCCCTCAGTCTCGGTATTTATTGCAATTCTCA 300
241 CGTATAATATAGGAATTCCAAGTTTGGGAGTCAGAGCCATAATAACGTAAGAGT
241 23 A Y Y I L K G S K T P Q S R Y L F A F S
241 TGCTTTAAGTTGGATCTTCTTGGAGAGGGCTGAAGCTGCATTGTTGCCCTGTCAAGATTAT
301 ACCAAATTCAACCTAGAAGAACCTCTCCGACTTCGACGTAACAACGGACACTTCTAATA 360
301 C F K L D L L G E A E A A L L P C E D Y
301 34 GCTGAAGAAGTTCTGGTGGTGCAGCTGGCATTATCTTCTTGGTCTTATATATAGATAT 420
361 CGACTTCTTCAAGGACCAACCACGTCGACCCGTAATAGAAGAACGAGAATATATATCTATA
361 34 A E E V P G G A A G H Y L L G L I Y R Y
361 45

FINGERPRINT

TCTGGGAGGAAGAACTGTTCAATAACAGTTAGGATGGCATTGTCATTGATCCATTG
421 -----+-----+-----+-----+-----+-----+-----+-----+-----+-----+
AGACCCCTCCCTCTTGACAAGTTATGTTGTCAAATCCTACCGTAACAGTAAACTAGGTAAAC

S G R K N C S I Q Q F R M A L S F D P L
56
TGTGGGAAGCATATGGAGAACCTTGTAGTTAGTGGCGCTGAAGAAGCCTAACAGT
481 -----+-----+-----+-----+-----+-----+-----+-----+-----+-----+
ACAACCCCTTCGTATAACCTCTTGAAACATCAAATCCACGGCGACTTCTTCGGAGTTGTCAA
56
C W E A Y G E L C S L G | A A E E A S T V

TTCGGGAATGTTGCTTCCCAGCGTCTTAAAACCTTGTGTAGAACAAAGAATAAGCTTCTCA
541 -----+-----+-----+-----+-----+-----+-----+-----+-----+-----+
AAGCCCTAACAGAAGGGTCCGAGAATTITGAACACATCTTGTTCCTATTGAAAGAGT

F G N V A S Q R L K T C V E Q R I S F S

GAAGGAGCAACCATAAACAGATTACAGATTCTGATAAGGCCTTAAAGATAACAGTTA
601 -----+-----+-----+-----+-----+-----+-----+-----+-----+-----+
CTTCCTCGTTGGTATCTGGTCTAATGTCTAACAGACTATTCCGGATTTCATGTCCAAT

E G A T I D Q I T D S D K A L K D T G L

TCGCAAACAGAACACATTCCAGGAGAGAACCAACAAGATCTGAAAATTATGCAGCAGCCT
661 -----+-----+-----+-----+-----+-----+-----+-----+-----+-----+
AGCGTTTGTCTTGTAAAGGTCTCTCTGGTTGTCTAGACTTTAAACGTCGTCCGA

S Q T E H I P G E N Q Q D L K I M Q Q P

GGAGATATTCCACCAAATACTGACAGGAACTTAGTACAAACGGATGGACTTGAACACA
721 -----+-----+-----+-----+-----+-----+-----+-----+-----+-----+
CCTCTATAAGGTGGTTATGACTGTCCGTTGAATCATGTTGCCTACCTGAACTTGTGT

G D I P P N T D R Q L S T N G W D L N T
67
CCTTCTCCAGTGCTTTACAGGTAAATGGATGCTCCACCGCCTCTGCTTCTTAAGAATATG
781 -----+-----+-----+-----+-----+-----+-----+-----+-----+-----+
GGAAGAGGTCAAGAAAATGTCCATTACCTACGGAGTGGCGGAGACGAAGAATTCTTATAC
67
P S P V L L Q V M D A P P P L L L K N M

CGTCGTCCAGCAGTGGAAAGGATCTTGATGTCTGTACATGGAGTGCCTGCGTCAAGA
841 -----+-----+-----+-----+-----+-----+-----+-----+-----+-----+
GCAGCAGGTGGTCAACCTTCCTAGAAACTACAGACATGTACCTCACGCACACGGCAGCTTCT

R R P A V E G S L M S V H G V R V R R R

7|8

AACTTTTTAGTGAAGAATTGTCAGCAGAGGCTAAGAAGAACCTGGGGCCCGTAGT
901 TTGAAAAAAATCACTTCTTAACAGTCGTCTCCGAGTTCTTAGACCCCCGGGGCATCA
N F F S E E L S A E | A Q E E S G R R R S
GCTAGAATAGCAGCAAGGAAAAAGAACCTATGTCGCAGTCATTGGAAAAGATTCCTAT
961 CGATCTTATCGTCGTTCCCTTTCTTAGGATAACAGCGTCAGTAAACCTTTCTAAGGGTA
A R I A A R K K N P M S Q S F G K D S H
TGGTTACATCTTCACCTTCCGAGTCAAACTATGCACCTTCTCTTCCTCGATGATGGAA
1021 ACCAATGTAGAAAGTGGAAAGGCTCAGTTGATACTGGAAGAGAAAGGAGCTACTAACCT
W L H L S P S E S N Y A P S L S S M I G
AAATGCAGAATCAAAGCAGCAAAGAACGGATTCTGATACCGTTACTCTAAATGATCCA
1081 TTTACGTCTTAGGTTCTCGTCTTCGCTAAGGACTATGGCAATGAGATTACTAGGT
K C R I Q S S K E A | I P D T V T L N D P
GCAACGACGTCAAGGCCAGTCTGTAAGTACACTGGAGCTCTGTTGATGATGAGAAAAG
1141 CGTTGCTGCAGTCCGGTCAGACATTCACTGTGACCTTCGAGACAACACTACTCCTTTTC
A T T S G Q S V S D T G S S V D D E E K
TCAAATCTAGTGAATCTTCCCCGGATCGTTCTAGCCTTATTTCTGGAATTCTAGAAGTG
1201 AGTTIAGGATCACTTAGAAGGGGCTAGCAAAGTCGAATAAGACCTAAAGTCTTCAC
S N P S E S S P D R F S L I S G I S E V
CTAGGCATTCTGAAAATTCTGGAGATGCCACAGGCATTACATATGTACAAGTGTAG
1261 GATCCGTAAGACTTTAAGAACCTCTACGGTGTCCGTAAATGTATACTGTTACAGTC
L G I L K I L G D G H R H L H M Y K C Q
9|

1321 10 | GAAGCTTTGGCATATCAAAGCTATCTCAGAAACAAATAACAAATAACACACTGGGTTCTC
 1380
 CTTCGAAACAACCGTATAGTTTCGATAGAGTCCTTGTTATGTTATGTGTGACCCAAGAG
 1381 10 | E A L L A Y Q K L S Q K Q Y N T H W V L
 1440
 10 | 11 ATGCAGETTGGAAAAGCATATTGAGCTACAGACTACTTCACCGCTGACTCTTCCTT
 1441
 TAGTCCAACCTTTCTGTATAAAACTCGATGTTCTGATGAAGTTGCCACTGAGAAGGAAA
 10 | 11 M Q | V G K A Y F E L Q D Y F N A D S S F
 ACTCTTGTCTCATAAAAGTATCCATTGCTTGAGGAATGGATACATACTCCACTGTT
 1500
 TGAGAACGAGTAGTTTCATAGGAATACGAAACCTTCTTACCTATGTATGAGGTGACAA
 1501
 T L A H Q K Y P Y A L E G M D T Y S T V
 1560
 11 | 12 CTTTATCACCTGAAAGAACAGATGAGGTTGGCTATCTGGCTCAGGAACGTGTTAGTT
 1561
 GAAATAGTGGACTTTCTCTACTCCAACCCGATAGACCGAGTCCTTGACTAAAGTCAA
 11 | 12 L Y | H L K E E M R L G Y L A Q E L I S V
 1561
 12 | 13 GATCGCCCTGTCTCCAGAACCTGGTGTGGAGTTGGAACTGTTACAGTTGGCTAAGGAT
 1620
 CTAGCGGACAGAGGTCTTACGACCACACGTCAACCTTGAACATGTCAAACGCATTCTTA
 1621
 12 | 13 D R E S P E S W | C A V G N C Y S L R K D
 1680
 CATGATACTGCTCTCAAAATGTTCAAGAGAGCTATCCAACGTAATGAAAGATTCAACATAT
 GTACTATGACGAGAGTTTACAAAGTCTCTCGATAGGTTGACTTACTTTCTAAGTGTATA
 1681
 H D T A L K M F Q R A I Q L N E R F T Y
 13 | 14 GCACATACCCCTTGTGGCCACGAGTTGGCCGATTGGAAAGAATTGGAGGATGGAGAGAGA
 1740
 CGTGTATGGAAACACCGGTGCTCAAACGGCGTAACCTTCTTAAGCTCCTACGTCTCT
 1741
 13 | 14 A H T L C G H E | F A A L E E F E D A E R
 1800
 TGCTACCGGAAGGCTCTGGCATAGATAACGAGACACTATAATGCATGGTACGGTCTTGG
 ACGATGGCCTTCCGAGACCCGTATCTATGCTCTGTGATATTACGTACCATGCCAGAACCT
 C Y R K A L G I D T R H Y N A W Y G L G -

ATGACCTATCTTCGTCAAGGAGAAATTGAGTTGGCAGCATCAATTCAACTGGCTCTC
 1801 -----+-----+-----+-----+-----+-----+-----+-----+-----+
 TACTGGATAGAACGAGTCCTCTTAAGCTCAAACGGTGTAGTTAAAGTTGACCGAGAG
 M T Y L R Q E K F E F A Q H Q F Q L A I
 CAAATAAATCCAAGATCTTCAGTCATCATGTGTTACTATGGAATGGCTTGATGAGTC
 1861 -----+-----+-----+-----+-----+-----+-----+-----+-----+
 GTTTATTAGGTTCTAGAAGTCAGTAGTACACAATGATAACCTTAACGAAACGTACTCA
 Q I N P R S S V I M C Y Y G I A L H E S
 1415
 AAGAGAAAACCGATGAGGCCTTGATGATGATGGAGAAGGCTGTACTCACTGATGCAAAGAAT
 1921 -----+-----+-----+-----+-----+-----+-----+-----+-----+
 TTCTCTTGCTACTCCGCAACTACTACTACCTCTTCCGACATGAGTGA
 1980 15
 K|R N D E A L M M M E K A V L T D A K N
 CCGCTCCCCAAGTACTACAACGCTCACATATTAAACCAGCCTAGGTGATTATCACAAAGCA
 1981 -----+-----+-----+-----+-----+-----+-----+-----+
 GGCGAGGGGTTCATGATGTTCCGAGTGTATAATTGGTCGGATCCACTAATAGTGTTCGTT
 P L P K Y Y K A H I L T S L G D Y H K A
 CAGAAAGTTTAGAAGAGCTCAAAGAATGTGCTCCTCAAGAAAGCAGTGTCCATGGATCG
 2041 -----+-----+-----+-----+-----+-----+-----+-----+-----+
 GTCTTTCAAAATCTTCTCGAGTTCTTACACGGAGGTTCTTCGTCACAGGTACGTAGC
 Q K V L E E L K E C A P Q E S S V H A S
 CTTGGCAAAATATAATCACATCAGCTAAAGCAATACGACAAAGCCGTGTTACATTTCGGCATT
 2101 -----+-----+-----+-----+-----+-----+-----+-----+-----+
 GAACCGTTTTATATGTTAGTCGATTTCGTTATGCTGTTCCGGACAATGTAAGCCGTA
 L G K I Y N Q L K Q Y D K A V L H F G I
 1516
 GCTTTGGATTTAAGCCCTCTCCATCTGATGCTGTCAAGATAAAAGGCTTACATGGAGAGG
 2161 -----+-----+-----+-----+-----+-----+-----+-----+-----+
 CGAAACCTAAATTGGAAAGAGGTAGACTACGACAGTTCTATTCCGAATGTAACCTCTCC
 2220 1516
 A L D L S P S P S D A V K I K | A Y M E R

CDC27B Gene Structure

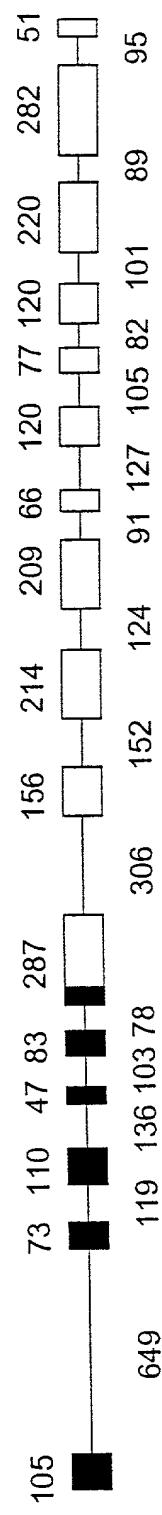


FIGURE 5

SEQ ID NO 6

Cdc27A1 1 - MMENLLANCVQKNNHFMFTNAIFLCELLLAQFPSEVNQLLLARCYLSNS
Cdc27B 1 - MEAMLV-DCVNNSLRHVFYKNAIFMCERLCAEFPSEVNQLLLATSYLQNN

SEQ ID NO 10

SEQ ID NO 6

Cdc27A1 51 - QAYSAYYILKGSKTPQSRYLFASFCKLDLLGEAEAALLP-CEDYAAEVIP
Cdc27B 50 - QAYSAYHILKGQTQMAQSRYLFALSCFQMDLLNEAESALCPVNEPGAE-IP

SEQ ID NO 10

Cdc27A1 100 - GGAAGHYLLGLIYRYSGRKNCSIQQFRMALSFDPLCWEAYGELCSLGAAE
Cdc27B 99 - NGAAGHYLLGLIY---KKNAA-QQFKQSLTIDPLLWAAYEELCILGAAE

SEQ ID NO 10

Cdc27A1 150 - EASTVFGNVASQRQLQKTCVEORISFSEG-ATIDQ--ITDSDKAL--KDTG
Cdc27B 144 - EATAVFGETAALSTIQKQYMQQ-LSTSGLNTYNEERNSTSTKNTSSEDYS

SEQ ID NO 10

Cdc27A1 194 - LSQTEHIPGENQQDLKIMQQPGDIPPNTDRQLSTNGWDLNTPSPVLLQVM
Cdc27B 193 - PROSKHTQSHGLKDISGNFHSHGVNGGV---SNMSFY-NTPSPVAAOLS

Cdc27A1 244 - D-APPPLL NMRRPAV-EG-SLMS-----VHG - VRVRRRNFFSE--
Cdc27B 238 - GIAPPPL-FRNFO-PAVANPNSSLTDSSPKSTVNSTLQAPRRKEVDEGKL

Cdc27A1 280 - -ELSAEAQEESG-RRRSARIAA-----RKKNPMSQSGKDSHWLHLSP
Cdc27B 286 - RKISGRLFSDSGPQR-SSRLSADSGANINSSVATVSGNVNNASKYLGGSK

SEQ ID NO 12

Cdc27A1 321 - SESNYAPSLSMIGKCRIQSSK-----EAIPD-TV-----TLNDPA
Cdc27B 335 - -----LSSLALRS-VTLRKGHSWANENM-DEGVRGEPPDDSRPNTAS

Cdc27A1 356 - TTSGQSVSDTGSSVDDEEKSNPSE--SSPDRFLSIS-GISEVLSILKILG
Cdc27B 375 - TTGSMASND---QEDETMSIGGIAMSSQT---ITIGVSEILNLRTLG

Cdc27A1 403 - DGHRHLHMYKQEAELLAYQKLSQKQYNTHWVLMQVGKAYFELDYFNADS
Cdc27B 417 - EGCRLSYMYRCQEALDTYMKLPHKHNTGWVLQVGKAYFELIDYLEAEK

Cdc27A1 453 - SFTLAHQKPYALEGMDTYSTVLYHLKEEMRLGYLAQELISVDRLSPESW
Cdc27B 467 - AFRLARLASPYCLEGMDIYSTVLYHLKEDMKLSYLAQELISTDRLAPQSW

Cdc27A1 503 - CAVGNCYSLRKDHDTALKMFQRAIQLNERFTYAHTLCGHEFAALEEFEDA
Cdc27B 517 - CAMGNCYSLQKDHEALKNFLRAVQLNPRFAYAHTLCGHEYTTLEDENG

Cdc27A1 553 - ERCYRKALGIDTRHYNAYGLGMTYLRQEKFQFAQHQFQLALQINPRSSV
Cdc27B 567 - MKSYQNALRVDTRHYNAYGLGMITYLRQEKFSEHHFRMAFLINPSSSV

Cdc27A1 603 - IMCYYYGIALHESKRNDEALMMMEKAVLTDAKNPLPKYYKAHILTSLGDYH
Cdc27B 617 - IMSYLGTSLHALKRSEEALEIMEQAIVADRKNPLPEMYQKANILIVCLERLD

Cdc27A1 653 - KAQKVLEELKECAPOESSVHASL-GKIYNNQLKQYDKAVLHFGLALDLSPS
Cdc27B 667 - EALEVLEELKEYAPSESSSVYA-LMGRIYKRRNMHDKAMLHFGLALDMKPP

SEQ ID NO 7

Cdc27A1 702 - PSDAVKIKAYMERLILPDELVTEENL
Cdc27B 716 - ATDVAAIKAAMEKLHVVPDEIDESP

FIGURE 6

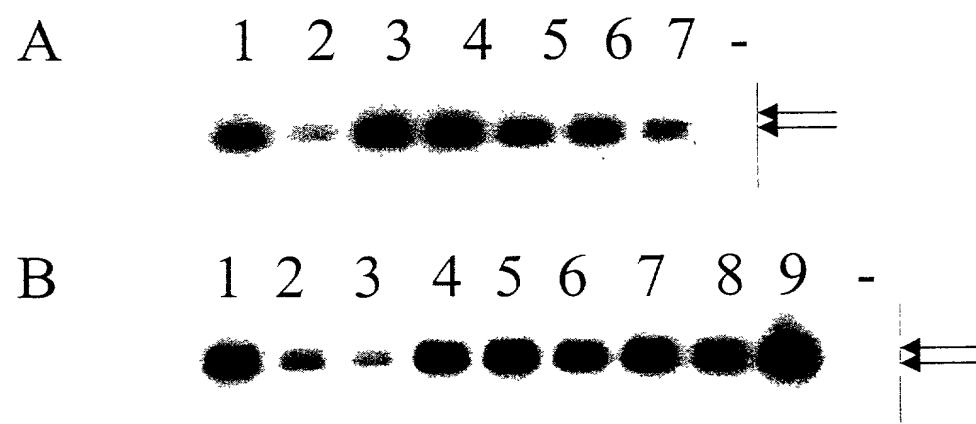


FIGURE 7

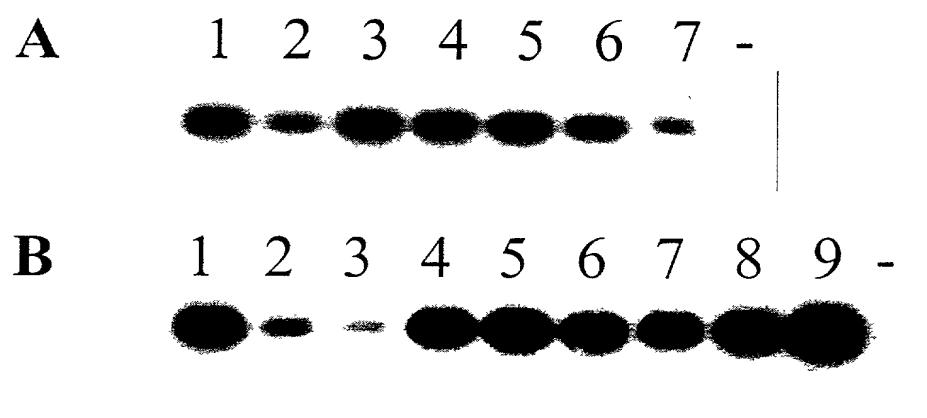


FIGURE 8